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Run on:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
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A_Geneseq_0601:*

// SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*

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1641
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTE

		ф				
Result No.	Score	Query Match Length DB	ength		ID	Description
<u>.</u>	1641	100.0	314	21	AAG45802	Arabidopsis thalia
N	1641	100.0	314	21	AAY93901	Amino acid sequenc
ω	1349	82.2	263	21	AAG45803	Arabidopsis thalia
4	1215	74.0	336	21	AAY93903	Amino acid sequenc
ъ	1215	74.0	391	21	AAY93904	Amino acid sequenc
თ	1213	73.9	1772	21	AAG52485	Arabidopsis thalia
7	1213	73.9	1776	21	AAG52484	Arabidopsis thalia
8	1213	73.9	1787	21	AAG52483	Arabidopsis thalia
9	916	55.8	180	21	AAG08083	Arabidopsis thalia
10	880	53.6	286	21	AAY44770	Soybean serine O-a
11	849.5	51.8	312	21	AAG39465	Arabidopsis thalia

			!	,		·	
Corn serine O-acet	7	21	175	39.0	640.5	4.5	
COL1	AAY57831	21	253	9	4	44	
μ	AAW35069	18	273	9	41.	43	
serine ac	805	18	273	9	٠	42	
cherichia coli	783	21	253	9	4	41	
thall	AAG08084	21	129	9	4	40	
ine a	AAW35068	18	273	φ	42.	39	
. coli serine	AAW35071	18	273	9	642.5	38	
. coli serine	AAW35077	18	273	ဖ	43.	37	
. coli serine	507	18	273	9	43.	36	
. coli	80	18	257	9	43.	35	
chia	AAY57827	21	253	9	644	34	
COLI	AAY57826	21	253	9	4	33	
ine	AAW35078	18	273	9		32	
. coli serine a	AAW35070	18	273	9		31	
cherichia coli	AAY57823	21	273	9		30	
oded b	AAY23827	20	273	9		29	
type Escher	AAW16618	18	273	9		28	
oli se	AAW35074	18	273	۰		27	
to	AAR37580	13	273	9		26	
serine	AAW35091	18	271	.0		25	
. coli serine	AAW35092	18	270	.0		24	
	AAW35093	18	268	.9	648.5	23	
coli	AAW35094	18	263	٠		22	
. coli	AAW35083	18	259	٩	•	21	
	AAW35084	18	258	·	•	20	
. coli	AAW35073	18	273	٠		19	
ş	AAY44771	21	157		ഗ	18	
Ci	AAY93905	21	359	ω.	₽	17	
ser	AAY44769	21	224		723.5	16	
	AAY44768	21	303	٠.	ω	15	
tiens balsami	AAY44767	21	294	:	4	14	
μ.	7	21	312	51.6	846.5	13	
s D	AAY93902	21	312	:	9.	12	

ALIGNMENTS

PR PR	PR	XX	PF XX	PD	X	ΡN	XX	20	××	ΚW	X	KW	××	DE	XX	×	AC	XX	ID .	RESULT									
19-APR-1999; 99US-0130077. 21-APR-1999; 99US-0130449.	٠.								••	25-FEB-1999; 99US-0121825.		25-FEB-2000; 2000EP-0301439.	06-SEP-2000.		EP1033405-A2.		Arabidopsis thaliana.			hybridisation assay; genetic mapping; gene expression control; promoter;		•	Arabidopsis thaliana protein fragment SEQ ID NO: 57548.	18-Oct-2000 (illsc entry)		AAG45802;		AAG45802 standard; Protein; 314 AA.	RESULT 1

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23-APR 1999 28-APR 1999 28-APR 1999 30-APR 1999 30-APR 1999 04-MAY 1999 06-MAY 1999 06-MAY 1999 14-MAY 1999 16-JUN 1999 27-MAY 1999 27-MAY 1999 27-MAY 1999 28-MAY 1999 18-JUN 1999 19-JUN 1999 20-JUN 1999 19-JUN 1999 20-JUN 1999 19-JUN 1999 20-JUN
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RESULT
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Best Local
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21-OCT-1999;
22-OCT-1999;
22-OCT-1999;
22-OCT-1999;
25-OCT-1999;
25-OCT-1999;
25-OCT-1999;
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26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
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21-OCT-1999;
21-OCT-1999;
21-OCT-1999;
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14-OCT-1999;
18-OCT-1999;
                                                                                                                                                                         glutathione;
                                                                                                                                                                                         Serine acetyltransferase; SAT; SAT3; transgenic plant; glutathione; methionine; nutrient value; plant-derived
                                                                                                                                                                                                                                                           Amino acid sequence of serine acetyltransferase (SAT) isoform SAT3.
                                                                                                                                                                                                                                                                                                      03-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                         AAY93901 standard; Protein; 314 AA.
                                                                                                                              Arabidopsis thaliana.
17-DEC-1999;
                                                                                     WO200036127-A1.
                                          22-JUN-2000
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hes 314;
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                                                                                                                                                                         viral resistance.
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990S-0161360.
990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
990S-0162142.
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99US-0159584.
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99US-0161405.
99US-0161406.
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99US-0160767.
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Matches 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents an isoform of serine acetyltransferase (SAT). The SAT polynucleotide is used to produce transgenic plants, which have increased production of cysteine, glutathione, methionine and their sulfur-containing derivatives. SAT catalyses conversion of serine to 0-acetylserine which is a precursor (by reaction with sulphide) for cysteine, itself a precursor for the other sulphur-containing compounds. The SAT polynucleotides and polypeptides are used to improve the nutrient value of plant-derived foods, and also (associated with the procursor of the production of plant-derived foods).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Increasing production of sulfur-containing compounds, e.g. cysteine or methionine, in plants, useful e.g. for improving nutritional value, by overexpressing serine acetyltransferase –
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 9; Page 50-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  increased production of glutathione) to improve resistance to stress
                                                 Protein identification; signal transduction pathway; metabolic pathway;
                                                                                                        18-OCT-2000
                                                                                                                                                        AAG45803 standard;
                          termination
                                                                           Arabidopsis thaliana protein fragment SEQ ID NO: 57549.
                                       hybridisation assay;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  DQTSYLTEWSDYVI 314
                                                                                                                                                                                                                                                                                                                            \verb|matcidtcrtg| ntg| dddsrfcciknffrpgfsvnrkihhtg| ieddddvwikmlee aksdv|
                                                                                                                                                                                                                        dqtsyltewsdyvi
                                                                                                                                                                                                                                                                         IGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARLIGGKENPRKHDKIPCLTM 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            314 AA;
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                          sequence
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                                                                                                                                                           Protein;
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                                      genetic mapping; gene expression control;
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                                                                                                              HDKIPCLIMDQTSYLTEWSDYVI 314
                                                                                                                                                          ESPEIIESTKODLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQNRKIVALLI 171
                                           hdkipcltmdqtsyltewsdyvi 263
                                                                             hpkigdgvligagscilgnitigegakigsgsvvvkdvparttavgnparliggkenprk\\
                                                                                      HPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARLIGGKENPRK 291
                                                                                                                                                   espeilestkqdliavkerdpacisyvhcflgfkgflacqahrlahtlwkqnrkivalli
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                                                                                                                                                                                                                                82.2%;
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Pred. No. 4e-123;
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glutathione;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Serine acetyltransferase; SAT; SAT1'; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of serine acetyltransferase (SAT) isoform SAT1'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                (SAT). The SAT polynuclectide is used to produce transgenic plants, which have increased production of cysteine, glutathione, methionine and their sulfur-containing derivatives. SAT catalyses conversion of serine to O-acetylserine which is a precursor (by reaction with sulphide) for cysteine, itself a precursor for the other sulphur-containing compounds. The SAT polynucleotides and polypeptides are used to improve the nutrient value of plant-derived foods, and also (associated with increased production of glutathione) to improve resistance to stress.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 14; Page 53-54; 69pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            overexpressing serine acetyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Increasing production of sulfur-containing compounds, e.g. cysteine methionine, in plants, useful e.g. for improving nutritional value,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
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                                                                                                                                                                                                                                                                                                                   1 MATCIDTCRTGNTQ------DDDSRFCCIKNFFRPGFS----VNRKIHHTQ--IED 44
                                                                                                                                                                                                                                                                                    \verb|maacidtcrtgkpqisprdsskhhddesgfrymnyfrypdrssfngtqtktlhtrplled| 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000-431603/37.
                                                                                                             -----DDDVWIKMLEEAKSDVKQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLP
                                                      vtlggtgkqcgdrhpkigdgvligagtcilgnitigegakigagsvvlkdvpprttavgn
                                                                                  VTLGGTGKQSGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGN
                                                                                                                                                                                                  SNTLFELFISVLEESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHT 158
parllggkdnpkthdkipgltmdqtshisewsdyvi
                           PARLIGGKENPRKHDKIPCLTMDQTSYLTEWSDYVI 314
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                                                                                                                                                                                                                                                                                                                                                                                                                         336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   methionine; nutri
viral resistance.
                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                               74.0%;
                                                                          nutrient value; plant-derived food;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Derose
                                                                                                                                                                                                                                                                                                                                                   31; Mismatches
                                                                                                                                                                                                                                                                                                                                                               Score 1215; DB 21;
Pred. No. 6.2e-110;
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                                                                                                                                                                                                                                                                                                                                                                                 Length 336;
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Best Local
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                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 54-56; 69pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    overexpressing serine acetyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Increasing production of sulfur-containing compounds, e.g. cysteine or methionine, in plants, useful e.g. for improving nutritional value, by
Droux M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-DEC-1998;
                                                                                                             116 Idrdaevddvwakireeaksdiakepivsayyhasivsqrsleaalantlsvklsnlnlp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serine acetyltransferase; SAT; SAT1; transgenic plant; cysteine; glutathione; methionine; nutrient value; plant-derived food; glutathione; viral resistance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of serine acetyltransferase (SAT) isoform SAT1.
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                                                                                                                                                                                                                                                   Local
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                                                                                                                              -----DDDVWIKMLEEAKSDVKQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000-431603/37.
DB; AAA47176.
                                                                                                                                                                                                                                                h 74.0%;
Similarity 72.0%;
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                                                                                                                                                                                                                                                                                                        391 AA;
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                                                                                                                                                                                                                                   31; Mismatches
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Pred. No. 7.7e-110;
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01-JUN-1999;
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19-MAY-1999;
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05-MAR-1999;
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                                                     99US-0136392.
99US-0136782.
99US-0137222.
99US-0137528.
99US-0137502.
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99US-0135124.
99US-0135353.
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99US-0130891.
99US-0131449.
99US-0132048.
99US-0132407.
99US-0132484.
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99US-0138094
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99US-0136021
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99US-0128234.
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99US-0134256
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QΥ
                                      Query Match 73.9%;
Best Local Similarity 71.4%;
Matches 240; Conservative
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1 MATCIDTCRTGNTQ------DDDSRFCCIKNFFRPGFS----VNRKIHHTQ--IED 44
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990S-0161361.
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33; Mismatches
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1.1e-108;
hes 41;
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                                               Indels
                                                                          1772;
                                               22;
                                               Gaps
                                                4;
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10-JUN-1999;
16-JUN-1999;
17-JUN-1999;
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19-JUL-1999;
10-JUL-1999;
10-JU

990S-0138847 990S-0139452 990S-0139453 990S-0139456 990S-0139456 990S-0139459 990S-0139460 990S-0139461 990S-0139461 990S-0139462 990S-0139462 990S-0139750 990S-0140852 990S-0140853 990S-01412877 990S-01412877 990S-01412877 990S-014290 990S-0142920 990S-0144333 990S-0144331 990S-0144331 990S-0144332 990S-0144333 990S-0144333 990S-0144331 990S-0144331 990S-0144331 990S-0144331 990S-0144331 990S-0144331 990S-0144331 990S-0145086 990S-0145086 990S-0145086 990S-0145086 990S-0145086 990S-0145086 990S-0145086 990S-0145086 990S-0145089 990S-0145086 990S-0147038 990S-0147204 990S-0147204 990S-0147303 990S-0147303 990S-0147303 990S-0147303

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14-MAY-1999

14-MAY-1999
                                                                                                                                                                                                                                                                                                                          Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                            25-FEB-2000; 2000EP-0301439.
                                                                                                                                                                                                                                                                               06-SEP-2000.
                                                                                                                                                                                                                                                                                               EP1033405-A2.
                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana protein fragment SEQ ID NO: 66721.
                                                                                                                                                                                                                                                                                                                                                                                                    AAG52484;
                                                                                                                                                                                                                                                                                                                                                                                                                   AAG52484 standard;
                                                                                                                                                                                                                                                                                                                                                                                 18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          279 PARLIGGKENPRKHDKIPCLTMDQTSYLTEWSDYVI 314
||||:|||:||:||:||||||:::|||||:::
341 parllggkdnpkthdklpgltmdqtshisewsdyiv 376
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99US-0130891

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99US-013485

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99US-0134219

99US-01342768
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   19-JUL-1999

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21-JUN-1999;
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28-MAY-1999;
01-JUN-1999;
03-JUN-1999;
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18-JUN-1999;
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99US-0141287.
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99US-0136021.
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28-JUL 02-AUG 02-AUG 02-AUG 03-AUG 04-AUG 04-AUG 05-AUG 05-AUG 06-AUG 06-AUG 09-AUG 09-AUG 11-AUG

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Matches
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26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
25-FEB-1999

05-MAR-1999

09-MAR-1999

23-MAR-1999

25-MAR-1999

20-MAR-1999

01-APR-1999

06-APR-1999

06-APR-1999

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16-APR-1999

11-APR-1999

21-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999
                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter
                                                                                                                                                                                                                                                   Arabidopsis thaliana protein fragment SEQ ID
                                                                                                                                                                                                                                                                                      AAG52483;
                                                                                                                                                                                                                                                                                                        AAG52483 standard;
                                                                                                                                                             06-SEP-2000
                                                                                                                                                                              EP1033405-A2
                                                                                                                                                                                              Arabidopsis thaliana
                                                                                                                                                                                                                termination sequence.
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                                                                                                                                           25-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                 PARLIGGKENPRKHDKIPCLIMDQTSYLTEWSDYVI ||||:||:||: ||||| ||||||:::|||||:::parllggkdnpkthdkipgltmdqtshisewsdyiv
                                                                                                                                                                                                                                                                                                                                                                                                                                                          \verb|maacidtcrtgkpqisprdsskhhddesgfrymnyfrypdrssfngtqtktlhtrplled|
                                                                                                                                                                                                                                                                                                                                                                                              VTLGGTGKQSGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGN
                                                                                                                                                                                                                                                                                                                                                                                                                       \verb|vtlggtgkqcgdrhpkigdgvligagtcilgnitigegakigagsvvlkdvpprttavgn|
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240; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0161360.
99US-0161361.
99US-0161920.
99US-0161992.
99US-0161993.
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990S-0128234.

990S-012845.

990S-0130077.

990S-0130049.

990S-0130049.

990S-0130891.

990S-0131449.
                                                                                                                                                                                                                                                                                                        Protein; 1787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1213; DB 21;
Pred. No. 1.1e-108;
33; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                    380
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21-CCT-1999

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990S-014723 990S-0147416 990S-0147416 990S-0147743 990S-0148311 990S-0148311 990S-0148364 990S-0149368 990S-0149368 990S-0149922 990S-0149922 990S-0149922 990S-0150566 990S-0151065 990S-0151066 990S-0151066 990S-0151066 990S-0151066 990S-0151066 990S-0151066 990S-0151068 990S-0151068 990S-0151068 990S-0151068 990S-0151765 990S-015363 990S-0158779 990S-0155486 990S-0158779 990S-0158783 990S-0158793 990S-0158793 990S-0158793 990S-0158793 990S-0158369 990S-0158369 990S-0159331 990S-0159331 990S-0159331 990S-0159331 990S-0159331 990S-0159331 990S-0159331 990S-0159331 990S-0159331	

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Best Local Sim
Matches 240;
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29-OCT 1999
                                                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
      25-FEB-1999;
05-MAR-1999;
                                                                                                                                                       Arabidopsis thaliana protein fragment SEQ ID NO: 5483.
                                                                                                                                                                           17-OCT-2000 (first entry)
                                    25-FEB-2000; 2000EP-0301439.
                                                       06-SEP-2000.
                                                                                               Arabidopsis thaliana
                                                                                                                                                                                                                      AAG08083 standard;
                                                                                                                                                                                                                                                                      279 PARLIGGKENPRKHDKIPCLIMDQTSYLTEWSDYVI 314
||||:|||:||:|||||||||:::|||||:::
356 parliggkdnpkthdkipgltmdqtshisewsdyiv 391
                                                                                                                                                                                                                                                                                                                                                    219
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                                                                                                                                                                                                                                                                                                            maacidtcrtgkpqisprdsskhhddesgfrymnyfrypdrssfngtqtktlhtrplled 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 71.4
40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0160741
99US-0160767
99US-0160770
99US-0160814
99US-0160815
99US-0160980
99US-0160980
99US-0161404
99US-0161405
99US-0161405
99US-0161406
99US-0161406
99US-0161406
99US-0161359
99US-0161359
99US-0161920
99US-0161920
     99US-0121825.
99US-0123180.
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71.4%;
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%; Pred. No. 1.16
33; Mismatches
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1.1e-108;
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                                                                                                                                                                                                                                                                                                                                  278
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  18-JUN-1999
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17-JUN-1999
         99US-0142055.
99US-0142390.
99US-0142803.
99US-0142920.
99US-0142977.
99US-0143542.
                                                                    9908-013722

9908-0137522

9908-0137502

9908-0137502

9908-0138540

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9908-0138452

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990S-0132485
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990S-0134276
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15-JUL-1999; 16-JUL-1999; 16-JUL-1999; 19-JUL-1999; 19-JUL-1999;

19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999;

20-JUL-1999; 20-JUL-1999; 21-JUL-1999; 21-JUL-1999; 21-JUL-1999; 22-JUL-1999; 22-JUL-1999;

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RESULT 10
AAY44770
ID AAY447
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  Query Match 55.8%;
Best Local Similarity 97.2%;
Matches 175; Conservative
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07-OCT-1999;
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12-OCT-1999;
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18-0CT
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                                                                                                           Serine O-acetyltransferase; sulphate assimilation; O-acety soybean; clone srl.pk0162.a9; cysteine formation; marker; plant breeding; transgenic plant.
                                                                                                                                                                             04-MAY-2000 (first entry)
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14-OCT-1999;
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14-JUL-1998;
                       13-JUL-1999;
                                            27-JAN-2000
                                                                  WO200004167-A2
                                                                                                                                                         Soybean serine
                                                                                                                                                                                                                         AAY44770 standard; Protein; 286 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-OCT-1999
                                                                                                                                                                                                                                                                                         121 KQDLIAVKERDPACISYVHCELGFKGFLACQAHRIAHTLMKQNRKIVALLIQNRVSESFA
                                                                                                                                                                                                                                                                               121 kqdliavkerdpacisyvhcflgfkgflacqahriahtlwkqnrkivalliqnrvsesfa
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99US-0158029

99US-0158236

99US-0159294

99US-0159295

99US-0159295

99US-0159330

99US-0159331

99US-0159584

99US-0160767

99US-0160767

99US-0160768

99US-0160768
                      99WO-US15872.
                                                                                                                                                         O-acetyltransferase-1.
  98US-0092833
                                                                                                                                                                                                                                                                                                                                                                                                               Score 916; DB 21;
Pred. No. 3.1e-81;
2; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                  O-acetylserine;
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9908-0144005
9908-0144085
9908-0144332
9908-0144333
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9908-0144814
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27-JUL-1999
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29-AUG-1999
21-AUG-1999
21-AUG

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RESULT 11
AAG39465
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Best Local Similarity
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                                                                                                          Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                               Arabidopsis thaliana protein fragment SEQ ID NO: 48833.
                                                                                                                                                                                                                                                                                                         AAG39465 standard; Protein; 312 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O-acetyltransferase. Serine O-acetyltransferase converts serine to O-acetylserine, that is involved in the formation of cysteine. This sequence is used as a probe to isolate other plant sulphate assimilation proteins, for genetic and physical mapping of related genes and as markers of traits linked to the gene. This is useful for plant breeding. It is also used to create transgenic plants with altered levels of serine O-acetyltransferase, or found in cell types or developmental stages in which they are not normally found.
                                                                     Arabidopsis thaliana
                                                                                                                                                                                                                              18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the serine O-acetyltransferase, a sulphate assimilation protein isolated from soybean. This is obtained from srl cDNA library, from clone srl.pk0162.a9, derived from soybean root library. It has 87% sequence identity to Citrullus lanatus serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid fragment encoding a sulfate assimilation protein in plants, useful as probes to isolate genes encoding homologous proteins from other.plant species -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; Page 38-39; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       255 vggkekpskhedvpgesmdhtsfisewsdyii 286
                                                                                                                                                                                                                                                                                                                                                                                                                          283 IGGKENPRKHDKIPCLTMDQTSYLTEWSDYVI 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAZ50087.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FELFISVLEESPEIIESTKODLIAVKERDPACISYVHCELGFKGFLACQAHRIAHTLWKQ 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTGKQSGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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06-MAY-1999
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19-MAY-1999
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21-MAY-1999
21-JUN-1999
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18-JUN-1999;
18-JUN-1999;
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04-MAY-1999;
05-MAY-1999;
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19-APR-1999;
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06-APR-1999
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                                                                                                                                                                                                         990S-0138540

990S-013919

990S-0139452

990S-0139453

990S-0139453

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99US-0141842.
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99US-0139899.
99US-0140353.
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99US-0137222.
99US-0137528.
99US-0137502.
99US-0137724.
99US-0138094.
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99US-0136021.
99US-0136392.
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99US-0134218.
99US-0134219.
99US-0134221.
99US-0134370.
99US-0134768.
99US-0134941.
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99US-0132486.
99US-0132487.
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99US-0129845.
99US-0130077.
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99US-0135353.
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99US-0130510.
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뭥 20 밁 Š DЬ Ş Дb δÃ 밁 Qy

06-JUL-1999 08-JUL-1999 09-JUL-1999 12-JUL-1999 13-JUL-1999 14-JUL-1999 15-JUL-1999 16-JUL-1999 16-JUL-1999 19-JUL-1999 19-JUL-1999 19-JUL-1999 19-JUL-1999 19-JUL-1999 19-JUL-1999 19-JUL-1999 19-JUL-1999

> 99US-0142390. 99US-0142803. 99US-0142920. 99US-0142977. 99US-0143542.

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Best Local S
Matches 160
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24-SEP-1999;
28-SEP-1999;
29-SEP-1999;
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14-OCT-1999;
14-OCT-1999;
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13-OCT-1999;
13-OCT-1999;
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22-OCT-1999;
22-OCT-1999;
22-OCT-1999;
25-OCT-1999;
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25-OCT-1999;
26-OCT-1999;
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28-OCT-1999;
29-OCT-1999;
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21-OCT-1999;
21-OCT-1999;
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14-OCT-1999;
14-OCT-1999;
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07-OCT-1999;
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05-OCT-1999;
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Amino acid sequence
                                       03-OCT-2000 (first entry)
                                                                          AAY93902;
                                                                                                                 AAY93902 standard;
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| || :| :|| ||:::||||:
285 kptihdeecpgesmdhtsfisewsdyii 312
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99US-0160770.
99US-0160814.
99US-0160815.
99US-0160815.
99US-0160980.
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99US-0156596

99US-0156596

99US-0157117

99US-0157865

99US-0157865

99US-0158029

99US-0158232

99US-0158232

99US-0159294

99US-0159293

99US-0159293

99US-0159331

99US-0159331

99US-0159331

99US-0159331

99US-0159331

99US-0159637

99US-0159637
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99US-0161405.
99US-0161406.
99US-0161359.
99US-0161350.
99US-0161361.
99US-0161920.
99US-0161920.
99US-0161993.
99US-0161993.
                                                                                                                 Protein; 312
 of serine acetyltransferase (SAT) isoform SAT3'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 849.5; DB 21;
; Pred. No. 2.1e-74;
45; Mismatches 62;
                                                                                                                     B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                          164
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99US-0144065
99US-0144085
99US-0144085
99US-0144331
99US-0144333
99US-0144333
99US-0144333
99US-0144333
99US-0144333
99US-0144804
99US-0145086
99US-0145086
99US-0145087
99US-0145087
99US-0145087
99US-0145145
99US-0145145
99US-0145218
99US-0145213
99US-0145213
99US-0146386
99US-0147204
99US-0146386
99US-014723
99US-014871
99US-014871
99US-0149723
99US-0149923
99US-0149923
99US-0151086
99US-0151086
99US-0151086
99US-0151086
99US-0153758
99US-0153758
99US-0153758
99US-0153758

20-JUL-1999 20-JUL-1999 20-JUL-1999 21-JUL-1999 21-JUL-1999 21-JUL-1999 22-JUL-1999 22-JUL-1999 22-JUL-1999 22-JUL-1999 22-JUL-1999 23-JUL-1999 23-JUL-1999 23-JUL-1999 23-JUL-1999 24-JUL-1999 27-JUL-1999 27-JUL-1999 27-JUL-1999 27-JUL-1999 28-JUL-1999 29-AUG-1999 01-AUG-1999 01-AUG-1999

10-NUG-1999;
11-AUG-1999;
12-AUG-1999;
13-AUG-1999;
13-AUG-1999;
16-AUG-1999;
20-AUG-1999;
20-AUG-1999;
20-AUG-1999;
20-AUG-1999;
20-AUG-1999;
23-AUG-1999;
23-AUG-1999;
23-AUG-1999;
24-AUG-1999;
25-AUG-1999;
27-AUG-1999;
27-AU

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AAG21076
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents an isoform of serine acetyltransferase (SAT). The SAT polynucleotide is used to produce transgenic plants, which have increased production of cysteine, glutathione, methionine and their sulfur-containing derivatives. SAT catalyses conversion of serine to 0-acetylserine which is a precursor (by reaction with sulphide) for cysteine, itself a precursor for the other sulphur-containing compounds. The SAT polynucleotides and polypeptides are used to improve the nutrient value of plant-derived foods, and also (associated with increased production of glutathione) to improve resistance to stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Increasing production of sulfur-containing compounds, e.g. cysteine or methionine, in plants, useful e.g. for improving nutritional value, by overexpressing serine acetyltransferase \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Serine acetyltransferase; SAT; SAT3'; transgenic plant; cysteine; glutathione; methionine; nutrient value; plant-derived food; glutathione; viral resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAA47174.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; Page 51-53; 69pp; French.
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17-OCT-2000
                        AAG21076;
                                             AAG21076 standard; Protein; 312
                                                                                                                                                                                                         165
                                                                                                                                                                                                                                                         105
                                                                                                         285 kptihdeecpgesmdhtsfisewsdyii 312
                                                                                                                                                                                                                                                                                108
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                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-431603/37.
                                                                                                                                                                                                      NPRKHD-KIPCLIMDQTSYLTEWSDYVI 314
                                                                                                                                                       SGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNPARLIGGKE
                                                                                                                                                                                                                                                                   SVLEESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQNRKIV 167
                                                                                                                                                                                                                                                                                                                                                       160;
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                                                                                                                                                                                                                                                                                                                                                                                                                   312 AA;
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Conservative
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                                                                                                                                                                                                                                                                                                                                                     51.8%; Score 849.5; DB 21; Length 312; 59.7%; Pred. No. 2.1e-74; tive 45; Mismatches 62; Indels 1;
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  28-APR-1999;
30-APR-1999;
30-APR-1999;
04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
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14 MAY 1999
18 MAY 1999
18 MAY 1999
20 MAY 1999
21 MAY 1999
24 MAY 1999
25 MAY 1999
26 MAY 1999
27 MAY 1999
07 JUN 1999
07 JUN 1999
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10 JUN 1999
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23-APR-1999;
23-APR-1999;
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08-APR-1999;
16-APR-1999;
19-APR-1999;
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25-MAR-1999;
29-MAR-1999;
01-APR-1999;
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Arabidopsis thaliana protein fragment SEQ ID NO: 23500
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Protein identification; signal transduction pathway; metabolic pathway; termination sequence. hybridisation assay; genetic mapping; gene expression control; promoter;

Arabidopsis thaliana.

EP1033405-A2

25-FEB-2000; 2000EP-0301439

25-FEB-1999; 05-MAR-1999; 09-MAR-1999; 99US-01 99US-01 99US-0121825 L23180

99US-0128234. 99US-0128714. 99US-0129845. 99US-01

99US-0132048. 99US-0132407. 99US-0132484. 99US-0132485. 99US-0130510. 99US-0130891. 99US-0131449.

9908-0130449

-0130077

99US-0132486. 99US-0132487. 99US-0132863. 99US-0134256.

99US-0134221 99US-0134370 99US-0134218 99US-0134219

99US-0134768.
99US-0135124.
99US-013553.
99US-0135629.
99US-0135629.
99US-0136782.
99US-0137528.
99US-0137528.
99US-0137528.
99US-0137528.
99US-0139454.
99US-0139452.
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99US-0139453.
99US-0139458.
99US-0139458.
99US-0139458.
99US-0139458.
99US-0139458.
99US-0139460.
99US-0139460.

(first entry)

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L-JUN-1999; 2-JUN-1999;

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Best Local S
Matches 160
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31-AUG-1999
31-AUG-1999
01-SEP-1999
10-SEP-1999
13-SEP-1999
15-SEP-1999
20-SEP-1999
20-SEP-1999
21-SEP-1999
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21-SEP-1999
21-SEP
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14-OCT 1999
14-OCT 1999
14-OCT 1999
14-OCT 1999
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21-OCT 1999
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28-OCT 1999
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12-OCT-1999
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hes 160;
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Similarity 59.750; Conservative
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990S-0151330

990S-0151330

990S-0153375

990S-0153758

990S-0153758

990S-0155139

990S-015559

990S-015559

990S-0157513

990S-0157753

990S-0158029

990S-0168029

990S-016981

990S-0160981

990S-0161404

990S-0161406

990S-0161406

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990S-0161359

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990S-0161361

990S-0161361

990S-0161920

990S-0161920

990S-0161920

990S-0161920

990S-0161920
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                                                                                                                                                                                                                                                                                                                                                63;
                                                                                                                                                                                                                                                                                                                                                                                 21;
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23-JUN-1999
23-JUN-1999
24-JUN-1999
24-JUN-1999
29-JUN-1999
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99US-0139817
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99US-0140823
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                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                              sulphate assimilation protein from Impatiens balsamia. This is obtained from clone ids.pk0030.b6, derived from I. balsamia developing seed, oracetyltransferase. Serine Oracetyltransferase serine oracetyltransferase serine oracetyltransferase converts serine to Oracetylserine, that is involved in the formation of cysteine. This sequence is used as a probe to isolate other plant sulphate assimilation proteins, for genetic and physical mapping of related genes and as markers of traits linked to the gene. This is useful for plant levels of serine Oracetyltransferase, or found in cell types or developmental erace is which them.
                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                developmental stages in which they are not normally found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid fragment encoding a sulfate assimilation protein in plants, useful as probes to isolate genes encoding homologous proteins from other plant species -
                220 TLGGTGKQSGDRHPKIGDGVLIGAGSCILGNITIGEGAKIGSGSVVVKDVPARTTAVGNP
                                           140 wsqnrkplslalqsriadvfsvdihpaarigkgvlldhatgvvigetavignnvsilhhv 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present amino acid sequence is the serine O-acetyltransferase, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 34; 44pp; English.
                                                                                                                                          100 NTLFELFISVLEESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTL 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine O-acetyltransferase; sulphate assimilation; clone ids.pk0030.b6; O-acetylserine; cysteine formation; marker; probe; plant breeding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Impatiens balsamia serine O-acetyltransferase.
                                                                                                          {\tt 80~tilydlflgvlssdaslraaavadlraarqrdpactsfshcllnykgflaiqaqrvahkm}
                                                                                                                                                                                                      42 IEDDDD--VWIKMLEEAKSDVKQEPILSNYYYASITSHRSLESALAHILSVKLSNLNLPS 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W0200004167-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Impatiens balsamia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY44767 standard; Protein; 294 AA
                                                                                                                                                                                                                                                                   Local
                                                              WKQNRKIVALLIQNRVSESFAVDIHPGAKIGKGILLDHATGVVIGETAVVGDNVSILHGV
                                                                                                                                                                          vedaeesgvwsqikaearrdaesepalasylystilshsslaaslsfhlgnklcsstlls
159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000-182432/16
                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                              294 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Allen SM,
                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0092833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US15872
                                                                                                                                                                                                                                                            51.6%;
57.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maxwell CA;
                                                                                                                                                                                                                                             51;
                                                                                                                                                                                                                                                         Score 846; DB 21;
Pred. No. 4.1e-74;
                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                        DB 21; Length 294;
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                                                                                                                                                                                                                                      Gaps
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Qy 밁

104 ELFISVLEESPEIIESTKQDLIAVKERDPACISYVHCFLGFKGFLACQAHRIAHTLWKQN 163

Matches 160; Query Match Best Local

Local

Similarity

Conservative

50.6%; Score 831; DB 21; Length 303; 59.0%; Pred. No. 1.2e-72; ative 44; Mismatches 63; Indels

Gaps

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AAY44768
ID AAY4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db
            The present sequence is the rice serine O-acetyltransferase, a sulphate assimilation protein. This is obtained from rir24 cDNA library, clone estrain 4360-R-62. It has 72% sequence leaf infected with Magaporthe grisea serine to G-acetyltransferase. Serine O-acetyltransferase. Serine O-acetyltransferase converts this sequence is used as a probe to isolate other plant sulphate assimilation proteins, for genetic and physical mapping of related genes and as markers of traits linked to the gene. This is useful for plant breeding. It is also used to create transgenic plants with altered tevels of serine O-acetyltransferase, or found in cell types or developmental stages in which they are not normally found.
Sequence
                                                                                                                                                                                                                       Claim 6; Page 35-36; 44pp; English.
                                                                                                                                                                                                                                                            New isolated nucleic acid fragment encoding a sulfate assimilation protein in plants, useful as probes to isolate genes encoding
                                                                                                                                                                                                                                                                                                                     N-PSDB; AAZ50085
                                                                                                                                                                                                                                                                                                                                                               Falco SC, Allen SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Serine O-acetyltransferase; sulphate assimilation; O-acetylserine; rice; clone rlr24.pk0069.all; cysteine formation; marker; probe; plant breeding; transgenic plant.
                                                                                                                                                                                                                                                  nomologous proteins from other plant species
                                                                                                                                                                                                                                                                                                                                                                                          (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                            14-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200004167-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rice serine O-acetyltransferase-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY44768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY44768 standard; Protein; 303 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 arlvggkdkpnvhadvpgesmdhtsfislwsdfvi 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280 ARLIGGKENPRKHDKIPCLTMDQTSYLTEWSDYVI 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             200 tlggtgkgggdrhpkigdgvligagatilgnvrigegakigagslvlidvppwttavgnp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15
                                                                                                                                                                                                                                                                                                                                  2000-182432/16.
303 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US15872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Encoded by GCG"
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